RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/757,415B
Source: IFW16
Date Processed by STIC: 1/4/06

ENTERED

IFW16

RAW SEQUENCE LISTING DATE: 01/04/2006
PATENT APPLICATION: **US/09/757,415B** TIME: 14:13:49

Input Set : **A:\2459-1-002N SEQLIST.TXT**
Output Set: **N:\CRF4\01042006\I757415B.raw**

<110> APPLICANT: Zhou, Ming-Ming
Goldfarb, Mitchell
<120> TITLE OF INVENTION: Methods of Identifying Modulators of the FGF Receptor
<130> FILE REFERENCE: 2459-1-002N
<140> CURRENT APPLICATION NUMBER: 09/757,415B
<141> CURRENT FILING DATE: 2001-01-09
<150> PRIOR APPLICATION NUMBER: 60/175,867
<151> PRIOR FILING DATE: 2000-01-12
<160> NUMBER OF SEQ ID NOS: 33
<170> SOFTWARE: FastSEQ for Windows Version 4.0
<210> SEQ ID NO: 1
<211> LENGTH: 508
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 1

```
Met Gly Ser Cys Cys Ser Cys Pro Asp Lys Asp Thr Val Pro Asp Asn
 1               5                  10                  15
His Arg Asn Lys Phe Lys Val Ile Asn Val Asp Asp Asp Gly Asn Glu
            20                  25                  30
Leu Gly Ser Gly Ile Met Glu Leu Thr Asp Thr Glu Leu Ile Leu Tyr
        35                  40                  45
Thr Arg Lys Arg Asp Ser Val Lys Trp His Tyr Leu Cys Leu Arg Arg
    50                  55                  60
Tyr Gly Tyr Asp Ser Asn Leu Phe Ser Phe Glu Ser Gly Arg Arg Cys
65                  70                  75                  80
Gln Thr Gly Gln Gly Ile Phe Ala Phe Lys Cys Ala Arg Ala Glu Glu
                85                  90                  95
Leu Phe Asn Met Leu Gln Glu Ile Met Gln Asn Asn Ser Ile Asn Val
            100                 105                 110
Val Glu Glu Pro Val Val Glu Arg Asn Asn His Gln Thr Glu Leu Glu
        115                 120                 125
Val Pro Arg Thr Pro Arg Thr Pro Thr Thr Pro Gly Phe Ala Ala Gln
    130                 135                 140
Asn Leu Pro Asn Gly Tyr Pro Arg Tyr Pro Ser Phe Gly Asp Ala Ser
145                 150                 155                 160
Ser His Pro Ser Ser Arg His Pro Ser Val Gly Ser Ala Arg Leu Pro
                165                 170                 175
Ser Val Gly Glu Glu Ser Thr His Pro Leu Leu Val Ala Glu Glu Gln
            180                 185                 190
Val His Thr Tyr Val Asn Thr Thr Gly Val Gln Glu Glu Arg Lys Asn
        195                 200                 205
Arg Thr Ser Val His Val Pro Leu Glu Ala Arg Val Ser Asn Ala Glu
```

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Input Set : **A:\2459-1-002N SEQLIST.TXT**
Output Set: **N:\CRF4\01042006\I757415B.raw**

```
55     210                 215                 220
56 Ser Ser Thr Pro Lys Glu Glu Pro Ser Ser Ile Glu Asp Arg Asp Pro
57 225                 230                 235                 240
58 Gln Ile Leu Leu Glu Pro Glu Gly Val Lys Phe Val Leu Gly Pro Thr
59                 245                 250                 255
60 Pro Val Gln Lys Gln Leu Met Glu Lys Glu Lys Leu Glu Gln Leu Gly
61             260                 265                 270
62 Arg Asp Gln Val Ser Gly Ser Gly Ala Asn Asn Thr Glu Trp Asp Thr
63         275                 280                 285
64 Gly Tyr Asp Ser Asp Glu Arg Arg Asp Ala Pro Ser Val Asn Lys Leu
65     290                 295                 300
66 Val Tyr Glu Asn Ile Asn Gly Leu Ser Ile Pro Ser Ala Ser Gly Val
67 305                 310                 315                 320
68 Arg Arg Gly Arg Leu Thr Ser Thr Ser Thr Ser Asp Thr Gln Asn Ile
69                 325                 330                 335
70 Asn Asn Ser Ala Gln Arg Arg Thr Ala Leu Leu Asn Tyr Glu Asn Leu
71             340                 345                 350
72 Pro Ser Leu Pro Pro Val Trp Glu Ala Arg Lys Leu Ser Arg Asp Glu
73         355                 360                 365
74 Asp Asp Asn Leu Gly Pro Lys Thr Pro Ser Leu Asn Gly Tyr His Asn
75     370                 375                 380
76 Asn Leu Asp Pro Met His Asn Tyr Val Asn Thr Glu Asn Val Thr Val
77 385                 390                 395                 400
78 Pro Ala Ser Ala His Lys Ile Glu Tyr Ser Arg Arg Arg Asp Cys Thr
79                 405                 410                 415
80 Pro Thr Val Phe Asn Phe Asp Ile Arg Arg Pro Ser Leu Glu His Arg
81             420                 425                 430
82 Gln Leu Asn Tyr Ile Gln Val Asp Leu Glu Gly Gly Ser Asp Ser Asp
83         435                 440                 445
84 Asn Pro Gln Thr Pro Lys Thr Pro Thr Thr Pro Leu Pro Gln Thr Pro
85     450                 455                 460
86 Thr Arg Arg Thr Glu Leu Tyr Ala Val Ile Asp Ile Glu Arg Thr Ala
87 465                 470                 475                 480
88 Ala Met Ser Asn Leu Gln Lys Ala Leu Pro Arg Asp Asp Gly Thr Ser
89                 485                 490                 495
90 Arg Lys Thr Arg His Asn Ser Thr Asp Leu Pro Met
91             500                 505
94 <210> SEQ ID NO: 2
95 <211> LENGTH: 822
96 <212> TYPE: PRT
97 <213> ORGANISM: Mus musculus
99 <400> SEQUENCE: 2
100 Met Trp Gly Trp Lys Cys Leu Leu Phe Trp Ala Val Leu Val Thr Ala
101  1               5                  10                  15
102 Thr Leu Cys Thr Ala Arg Pro Ala Pro Thr Leu Pro Glu Gln Ala Gln
103             20                  25                  30
104 Pro Trp Gly Val Pro Val Glu Val Glu Ser Leu Leu Val His Pro Gly
105         35                  40                  45
106 Asp Leu Leu Gln Leu Arg Cys Arg Leu Arg Asp Asp Val Gln Ser Ile
```

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Input Set : **A:\2459-1-002N SEQLIST.TXT**
Output Set: **N:\CRF4\01042006\I757415B.raw**

```
107     50                  55                  60
108 Asn Trp Leu Arg Asp Gly Val Gln Leu Val Glu Ser Asn Arg Thr Arg
109 65                  70                  75                  80
110 Ile Thr Gly Glu Glu Val Glu Val Arg Asp Ser Ile Pro Ala Asp Ser
111                 85                  90                  95
112 Gly Leu Tyr Ala Cys Val Thr Ser Ser Pro Ser Gly Ser Asp Thr Thr
113             100                 105                 110
114 Tyr Phe Ser Val Asn Val Ser Asp Ala Leu Pro Ser Ser Glu Asp Asp
115         115                 120                 125
116 Asp Asp Asp Asp Asp Ser Ser Ser Glu Glu Lys Glu Thr Asp Asn Thr
117     130                 135                 140
118 Lys Pro Asn Arg Arg Pro Val Ala Pro Tyr Trp Thr Ser Pro Glu Lys
119 145                 150                 155                 160
120 Met Glu Lys Lys Leu His Ala Val Pro Ala Ala Lys Thr Val Lys Phe
121                 165                 170                 175
122 Lys Cys Pro Ser Ser Gly Thr Pro Asn Pro Thr Leu Arg Trp Leu Lys
123             180                 185                 190
124 Asn Gly Lys Glu Phe Lys Pro Asp His Arg Ile Gly Gly Tyr Lys Val
125         195                 200                 205
126 Arg Tyr Ala Thr Trp Ser Ile Ile Met Asp Ser Val Val Pro Ser Asp
127     210                 215                 220
128 Lys Gly Asn Tyr Thr Cys Ile Val Glu Asn Glu Tyr Gly Ser Ile Asn
129 225                 230                 235                 240
130 His Thr Tyr Gln Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile
131                 245                 250                 255
132 Leu Gln Ala Gly Leu Pro Ala Asn Glu Thr Val Ala Leu Gly Ser Asn
133             260                 265                 270
134 Val Glu Phe Met Cys Lys Val Tyr Ser Asp Pro Gln Pro His Ile Gln
135         275                 280                 285
136 Trp Leu Lys His Ile Glu Val Asn Gly Ser Lys Ile Gly Pro Asp Asn
137     290                 295                 300
138 Leu Pro Tyr Val Gln Ile Leu Lys Thr Ala Gly Val Asn Thr Thr Asp
139 305                 310                 315                 320
140 Lys Glu Met Glu Val Leu His Leu Arg Asn Val Ser Phe Glu Asp Ala
141                 325                 330                 335
142 Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu Ser His His
143             340                 345                 350
144 Ser Ala Trp Leu Thr Val Leu Glu Ala Leu Glu Glu Arg Pro Ala Val
145         355                 360                 365
146 Met Thr Ser Pro Leu Tyr Leu Glu Ile Ile Ile Tyr Cys Thr Gly Ala
147     370                 375                 380
148 Phe Leu Ile Ser Cys Met Leu Gly Ser Val Ile Ile Tyr Lys Met Lys
149 385                 390                 395                 400
150 Ser Gly Thr Lys Lys Ser Asp Phe His Ser Gln Met Ala Val His Lys
151                 405                 410                 415
152 Leu Ala Lys Ser Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Asp
153             420                 425                 430
154 Ser Ser Ala Ser Met Asn Ser Gly Val Leu Leu Val Arg Pro Ser Arg
155         435                 440                 445
```

RAW SEQUENCE LISTING DATE: 01/04/2006
PATENT APPLICATION: US/09/757,415B TIME: 14:13:49

Input Set : A:\2459-1-002N SEQLIST.TXT
Output Set: N:\CRF4\01042006\I757415B.raw

```
156 Leu Ser Ser Ser Gly Thr Pro Met Pro Ala Gly Val Ser Glu Tyr Glu
157     450                 455                 460
158 Leu Pro Glu Asp Pro Arg Trp Glu Leu Pro Arg Asp Arg Leu Val Leu
159 465                 470                 475                 480
160 Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Leu Ala Glu
161                 485                 490                 495
162 Ala Ile Gly Leu Asp Lys Asp Lys Pro Asn Arg Val Thr Lys Val Ala
163             500                 505                 510
164 Val Lys Met Leu Lys Ser Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu
165         515                 520                 525
166 Ile Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile
167     530                 535                 540
168 Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile
169 545                 550                 555                 560
170 Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Gln Ala Arg
171                 565                 570                 575
172 Arg Pro Pro Gly Leu Glu Tyr Cys Tyr Asn Pro Ser His Asn Pro Glu
173             580                 585                 590
174 Glu Gln Leu Ser Ser Lys Asp Leu Val Ser Cys Ala Tyr Gln Val Ala
175         595                 600                 605
176 Arg Gly Met Glu Tyr Leu Ala Ser Lys Lys Cys Ile His Arg Asp Leu
177     610                 615                 620
178 Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn Val Met Lys Ile Ala
179 625                 630                 635                 640
180 Asp Phe Gly Leu Ala Arg Asp Ile His His Ile Asp Tyr Tyr Lys Lys
181                 645                 650                 655
182 Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu
183             660                 665                 670
184 Phe Asp Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val
185         675                 680                 685
186 Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Val
187     690                 695                 700
188 Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp
189 705                 710                 715                 720
190 Lys Pro Ser Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys
191                 725                 730                 735
192 Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu
193             740                 745                 750
194 Asp Leu Asp Arg Ile Val Ala Leu Thr Ser Ser Gln Glu Tyr Leu Asp
195         755                 760                 765
196 Leu Ser Ile Pro Leu Asp Gln Tyr Ser Pro Ser Phe Pro Asp Thr Arg
197     770                 775                 780
198 Ser Ser Thr Cys Ser Ser Gly Glu Asp Ser Val Phe Ser His Glu Pro
199 785                 790                 795                 800
200 Leu Pro Glu Glu Pro Cys Leu Pro Arg His Pro Thr Gln Leu Ala Asn
201                 805                 810                 815
202 Ser Gly Leu Lys Arg Arg
203             820
206 <210> SEQ ID NO: 3
```

RAW SEQUENCE LISTING DATE: 01/04/2006
PATENT APPLICATION: **US/09/757,415B** TIME: 14:13:49

Input Set : **A:\2459-1-002N SEQLIST.TXT**
Output Set: **N:\CRF4\01042006\I757415B.raw**

```
     207 <211> LENGTH: 22
     208 <212> TYPE: PRT
     209 <213> ORGANISM: Mus musculus
     211 <400> SEQUENCE: 3
     212 His Ser Gln Met Ala Val His Lys Leu Ala Lys Ser Ile Pro Leu Arg
     213  1               5                  10                  15
     214 Arg Gln Val Thr Val Ser
     215             20
     218 <210> SEQ ID NO: 4
     219 <211> LENGTH: 11
     220 <212> TYPE: PRT
     221 <213> ORGANISM: Artificial Sequence
     223 <220> FEATURE:
     224 <223> OTHER INFORMATION: Tyrosine phosphorylation peptide
W--> 226 <221> NAME/KEY: VARIANT
     227 <222> LOCATION: (9)...(9)
     228 <223> OTHER INFORMATION: Xaa is a phosphotyrosine
W--> 230 <400> 4
W--> 231 Leu Val Ile Ala Gly Asn Pro Ala Xaa Arg Ser
     232  1               5                  10
     235 <210> SEQ ID NO: 5
     236 <211> LENGTH: 16
     237 <212> TYPE: PRT
     238 <213> ORGANISM: Artificial Sequence
     240 <220> FEATURE:
     241 <223> OTHER INFORMATION: Consensus sequence
W--> 243 <221> NAME/KEY: VARIANT
     244 <222> LOCATION: (2)...(3)
     245 <223> OTHER INFORMATION: Xaa = Any Amino Acid
W--> 247 <221> VARIANT
     248 <222> LOCATION: (5)...(7)
     249 <223> OTHER INFORMATION: Xaa = Any Amino Acid
W--> 251 <221> VARIANT
     252 <222> LOCATION: (9)...(9)
     253 <223> OTHER INFORMATION: Xaa = Any Amino Acid
W--> 255 <221> VARIANT
     256 <222> LOCATION: (11)...(11)
     257 <223> OTHER INFORMATION: Xaa = Any Amino Acid
W--> 259 <221> VARIANT
     260 <222> LOCATION: (13)...(13)
     261 <223> OTHER INFORMATION: Xaa = Any Amino Acid
W--> 263 <221> VARIANT
     264 <222> LOCATION: (15)...(15)
     265 <223> OTHER INFORMATION: Xaa = Any Amino Acid
W--> 267 <400> 5
W--> 268 Val Xaa Xaa Leu Xaa Xaa Xaa Ile Xaa Leu Xaa Arg Xaa Val Xaa Val
     269  1               5                  10                  15
     272 <210> SEQ ID NO: 6
     273 <211> LENGTH: 4
```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/04/2006
PATENT APPLICATION: **US/09/757,415B** TIME: 14:13:50

Input Set : **A:\2459-1-002N SEQLIST.TXT**
Output Set: **N:\CRF4\01042006\I757415B.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 9
Seq#:5; Xaa Pos. 2,3,5,6,7,9,11,13,15
Seq#:6; Xaa Pos. 3,4
Seq#:7; Xaa Pos. 8

VERIFICATION SUMMARY DATE: 01/04/2006
PATENT APPLICATION: **US/09/757,415B** TIME: 14:13:50

Input Set : **A:\2459-1-002N SEQLIST.TXT**
Output Set: **N:\CRF4\01042006\I757415B.raw**

L:226 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:230 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:243 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:247 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:251 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:255 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:259 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:263 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:267 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:280 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:284 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:288 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:301 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:305 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:306 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0